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(FILE 'HOME' ENTERED AT 12:44:39 ON 14 MAR 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 12:44:50 ON 14 MAR 2006

L1 280834 SEA ABB=ON PLU=ON METHYLAT? OR HYPERMETHYLAT? OR HYPOMETHYLAT?
L2 448038 SEA ABB=ON PLU=ON DAPK OR GSTP OR P15 OR MDR1 OR PROGESTERONE
OR CALCITONIN OR RIZ OR RARBETA
L3 2992 SEA ABB=ON PLU=ON L1 (P) L2
L4 277 SEA ABB=ON PLU=ON L1 (P) L2 (P) BREAST
L5 101 DUP REM L4 (176 DUPLICATES REMOVED)
L6 48 SEA ABB=ON PLU=ON L5 AND PD<2003
D IBIB AB 1-48

FILE 'STNGUIDE' ENTERED AT 12:48:13 ON 14 MAR 2006

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 12:58:10 ON 14 MAR 2006

E LEVENSON V/AU
L7 70 SEA ABB=ON PLU=ON "LEVENSON V"/AU OR "LEVENSON V V"/AU OR
("LEVENSON VICTOR"/AU OR "LEVENSON VICTOR V"/AU)
E GARTENHAUS R/AU
L8 200 SEA ABB=ON PLU=ON ("GARTENHANS RONALD"/AU OR "GARTENHAUS
R"/AU OR "GARTENHAUS R B"/AU OR "GARTENHAUS RON"/AU OR
"GARTENHAUS RON B"/AU OR "GARTENHAUS RONALD"/AU OR "GARTENHAUS
RONALD B"/AU)
L9 259 SEA ABB=ON PLU=ON L7 OR L8
L10 51 SEA ABB=ON PLU=ON L9 AND (BREAST OR METHYLAT? OR CANCER)
L11 30 DUP REM L10 (21 DUPLICATES REMOVED)
D IBIB AB 1-30
L12 31 SEA ABB=ON PLU=ON RIZ (P) L1
L13 15 DUP REM L12 (16 DUPLICATES REMOVED)
D IBIB AB 1-15
L14 645411 SEA ABB=ON PLU=ON HI
L15 121 SEA ABB=ON PLU=ON (RIZ1 OR RIZ?) (P) L1
L16 52 DUP REM L15 (69 DUPLICATES REMOVED)
L17 3 SEA ABB=ON PLU=ON L16 AND BREAST
D IBIB AB 1-3

FILE 'STNGUIDE' ENTERED AT 13:06:05 ON 14 MAR 2006

FILE HOME

FILE MEDLINE

FILE LAST UPDATED: 11 MAR 2006 (20060311/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).

See also:

<http://www.nlm.nih.gov/mesh/>
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE BIOSIS
FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNS) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 9 March 2006 (20060309/ED)

FILE CAPLUS

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FILE COVERS 1907 - 14 Mar 2006 VOL 144 ISS 12
FILE LAST UPDATED: 13 Mar 2006 (20060313/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply. They are available for your review at:

<http://www.cas.org/infopolicy.html>

FILE EMBASE

FILE COVERS 1974 TO 10 Mar 2006 (20060310/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

The updates on February 20 and 24, 2006, were incomplete due to a technical problem. The problem has been corrected, and the missing records were included in the update on March 3, 2006. If you received SDI results from the original updates on February 20 and 24, you will automatically be credited for the update that was rerun on March 3.

If you have any questions, please contact your STN Service Center.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE SCISEARCH

FILE COVERS 1974 TO 9 Mar 2006 (20060309/ED)

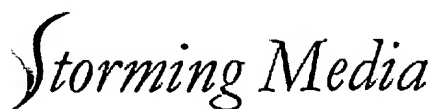
SCISEARCH has been reloaded, see HELP RLOAD for details.

FILE STNGUIDE

FILE CONTAINS CURRENT INFORMATION.

LAST RELOADED: Mar 10, 2006 (20060310/UP).

=>



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Epigenetic Changes in DNA Methylation in Breast Cancer

Authors: [Tim H. Huang](#); [MISSOURI UNIV-COLUMBIA](#)

Abstract: CpG island hypermethylation is a frequent epigenetic event in cancer. We have recently developed an array-based method, called differential methylation hybridization (DMH), allowing for a genome-wide screening of CpG island hypermethylation in breast cancer cell lines (Hum. Mol. Genet. 8: 459- 4%O, 1999) . In the present study, DMH was applied to screen 28 paired primary breast tumor and normal samples, and to determine whether patterns of specific epigenetic alterations correlate%with pathological parameters in the patients analyzed. Amplicons, representing a pool of methylated CpG DNA derived from these samples, were used as hybridization probes in an array panel containing 1, 104 CpG island tags. Close to 9 of these tags exhibited extensive hypermethylation in the majority of breast tumors relative to their normal controls, while others had little or no detectable changes. Pattern analysis in a subset of CpG island tags revealed that CpG island hypermethylation is associated with histological grades of breast tumors. Poorly differentiated tumors appeared to exhibit more hypermethylated CpG islands than their moderately or well-differentiated counterparts (Th-O.041) . This early finding lays the groundwork for population-based DMH study and demonstrates the need to develop a database for examining large-scale methylation data and for associating specific epigenetic signatures with clinical parameters in breast cancer.

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**Report
number:** A038783



Keywords relating to this report:

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